ResearchGate

See discussions, stats, and author profiles for this publication at: https://www.researchgate.net/publication/8614134

Molecular phylogenetic analyses indicate extensive morphological convergence between the “yeti” and primates

Article *in* Molecular Phylogenetics and Evolution · May 2004

DOI: 10.1016/j.ympev.2004.01.009 · Source: PubMed

CITATIONS
9

READS
2,098

3 authors:

Michel Milinkovitch
University of Geneva
430 PUBLICATIONS **9,787** CITATIONS

SEE PROFILE

Adalgisa Caccone
Yale University
694 PUBLICATIONS **13,143** CITATIONS

SEE PROFILE

George Amato
American Museum of Natural History
290 PUBLICATIONS **6,706** CITATIONS

SEE PROFILE

All content following this page was uploaded by Michel Milinkovitch on 24 June 2020.

The user has requested enhancement of the downloaded file.

Available online at www.sciencedirect.com
SCIENCE DIRECT®
Molecular Phylogenetics and Evolution 31 (2004) 1–3
MOLECULAR PHYLOGENETICS AND EVOLUTION
www.elsevier.com/locate/ympev

Molecular phylogenetic analyses indicate extensive morphological convergence between the "yeti" and primates☆

Michel C. Milinkovitch,[a,b,*] Aldagisa Caccone,[b] and George Amato[c]

[a] *Evolutionary Genetics, Institute of Molecular Biology and Medicine, Free University of Brussels (ULB), CP 300, B-6041 Gosselies, Belgium*
[b] *Molecular Systematics and Conservation Genetics, Yale University, New Haven, CT 06520-8106, USA*
[c] *Wildlife Conservation Society, New York 10460, USA*

Received 5 January 2004

1. Introduction

It is generally considered that most of our planet has been so extensively explored that very few, if any, living species of large vertebrate still remain to be discovered and described. Hence, the stir created by the recent description of ungulate species from Asia (Amato et al., 1998; Dung et al., 1993) is quite understandable. One large, probably mammalian, species that has been repeatedly sighted in Nepal—but for which no definitive remains or observable data has been collected so far—is the "ye-the," better known under the name "yeti" or "*Abominable Snowman*." Very little is known about the morphology of this enigmatic creature. The famous writer Peter Matthiessen notes that "The yeti is described most often as a hairy, reddish-brown creature with a rigid crown that gives it a pointed-head appearance; in size, despite the outsized foot [...] it has been likened to an adolescent boy, though much larger individuals have been reported" (Matthiessen, 1979, p. 119). This is perfectly consistent with the description given earlier by Haddock: "*A sort of enormous monkey ... with a huge head like a coconut*" (Hergé, 1960, p. 37). Behavioural data on the yeti is also very scarce but it probably can walk upright on its hind legs and it has been recorded stealing bottles of whisky from camp sites—a behaviour that has made it called "*the pithecanthropic pickpocket*" (Hergé, 1960, p. 37). It is usually assumed that the yeti is a primate while its exact phylogenetic position within that mammalian order is controversial. For example, a theory holds that "the yeti is a relict species of early man, driven long ago into dense forests by the surge of Homo sapiens that presumably eliminated more primitive hominids [...] its strange bestial foot [...] would seem to place it closer to a subhominid such as Gigantopithecus or even to apes ..." (Matthiessen, 1979, pp. 120–121).

"In 1992, Peter Matthiessen and photographer Thomas Laird were the first Westerners in over three decades to visit a remote region in the northernmost Himalaya. Located close to the boarder of Tibet, Sao Kohla is a mysterious valley outside of the main city of Lo Monthang. Here Matthiessen, Laird, and their Nepalese colleagues came upon some unusual foot prints in the snow, and were informed by locals that they were the prints of the Mehti (the local name for Yeti). Near a river at the bottom of the gorge, samples of twisted hair were recovered which were clearly identified as Mehti hair by their local guides (Matthiessen, 1995, p. 75–80). We were asked to analyze these samples, but first had to agree that any identification of a "new species" would have to be reported to the government of Nepal before publication. Using modified oligonucleotide primers L1091 and H1478 (Kocher et al., 1989), we successfully amplified and directly sequenced a fragment of the mitochondrial 12S ribosomal RNA gene (12S rRNA) from that sample. Surprisingly, comparison of the yeti sequence against all available 12S rRNA sequences identified a higher degree of similarity with a specific group of ungulates than with primates. We therefore aligned, using SOAP (Löytynoja and Milinkovitch, 2001), 12S rRNA sequences from representatives of that

☆ The study reported here represents a scientifically rigorous assessment of conflict between the published morphological characters and newly obtained molecular characters for a species of questionable validity. More significantly, however, this study indicates that evolutionary biologists need to retain a sense of humor in their efforts to reconstruct phylogenetic relationships. Happy April Fool's Day!

* Corresponding author. Fax: +32-2-650-9950.
E-mail address: mcmilink@ulb.ac.be (M.C. Milinkovitch).

doi:10.1016/j.ympev.2004.01.009

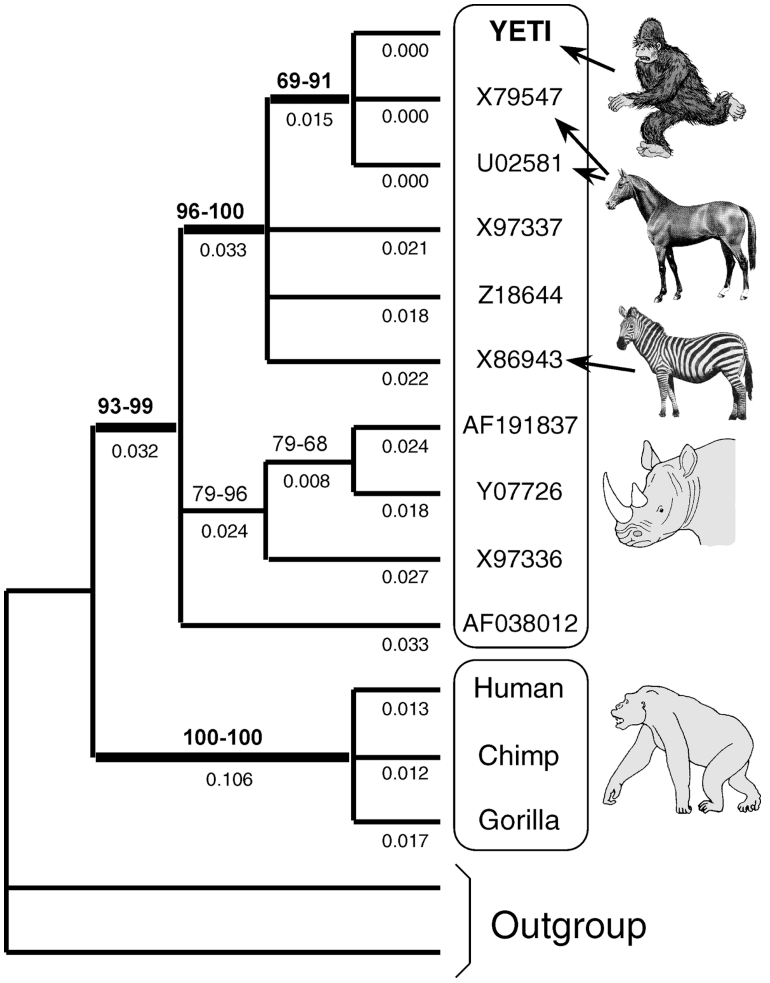

Fig. 1. Phylogenetic position of the yeti inferred from 12S rRNA data. Summary cladogram indicating branches supported by bootstrapping both under NJ (ML distances, transition/transvertion ratio estimated from the data) and unweighted MP. Bootstrap values >50% (MP–NJ) and branch lengths (NJ) are indicated above and below the branches, respectively. The yeti is separated from hominids by several well-supported branches (in bold). The species used are (GenBank Accession No. [*binomial name*, common name, mammalian order]): X79547 [*Equus caballus*, horse, Perissodactyla], U02581 [*Equus caballus*, horse, Perissodactyla], X97337 [*Equus asinus*, donkey, Perissodactyla], Z18644 [*Equus hemionus*, Kulan or wild ass, Perissodactyla], X86943 [*Equus grevyi*, Grevy's zebra, Perissodactyla], AF191837 [*Diceros bicornis*, black rhinoceros, Perissodactyla], X97336 [*Rhinoceros unicornis*, greater Indian rhinoceros, Perissodactyla], Y07726 [*Ceratotherium simum*, white rhinoceros, Perissodactyla], AF038012 [*Tapirus pinchaque*, tapir, Perissodactyla], D38112 [*Homo sapien*, human, primate], D38113 [*Pan troglodites*, chimpanzee, primate], D38114 [*Gorilla gorilla*, gorilla, primate]; outgroup taxa are Z18666 [*Physeter macrocephalus*, Giant Sperm Whale, Cetartiodactyla] and J01394 [*Bos taurus*, bovine, Cetartiodactyla]. The 12S sequence from the Yeti has been deposited at EMBL (www.ulb.ac.be/sciences/ueg/yeti/sequence). The analysed data set, available on request, is the strict consensus among the alignments obtained with 15 different sets of alignment parameters (weighted matrix, gap penalties from 13 to 17 by steps of 2, and extension penalties from 5 to 9 by steps of 2).

order together with the orthologous sequences from yeti, human, chimpanzee, gorilla, and two representatives of the order cetartiodactyla (e.g., Gatesy et al., 1999). The final alignment included 417 characters and is available, upon request, from the authors. The data set was phylogenetically analysed using maximum parsimony (MP), maximum likelihood (ML), and neighbour joining (NJ). We estimated the reliability of the various inferred clades by bootstrapping (Felsenstein, 1985) and Bremer support (Bremer, 1994). All analyses were performed with PAUP* (versions 4.0b4a) (Swofford, 1997). Fig. 1 shows the consensus between the NJ and MP 50% consensus bootstrap trees. The yeti sequence is separated from the hominid group by several nodes supported by high bootstrap values. Constraining the Yeti sequence to cluster with the hominids requires an increase in tree length estimated significant ($p < 0.05$) under KH tests (Kishino and Hasegawa, 1989). ML analyses yielded trees where the yeti is separated from hominids by the same branches as in Fig. 1.

All our analyses clearly indicate that the yeti is nested several nodes within a specific ungulate group (i.e., the perissodactyls, cf. Fig. 1) and, more specifically, forms a subclade with sequences U02581 and X79547 (cf. figure legend). These results demonstrate that extensive morphological convergences have occurred between the yeti

and primates. It is quite remarkable that Haddock already identified 44 years ago the correct phylogenetic position of the yeti (despite he had seen only footprints in the snow) when he yelled at it "You odd-toed ungulate!" (Hergé, 1960, p. 26).

References

Amato, G., Rabinowitz, A., Egan, M.G., 1998. Animal Conservation 2, 1–7.
Bremer, K., 1994. Cladistics 10, 295–304.
Dung, V.V. et al., 1993. Nature 363, 443–445.
Felsenstein, 1985. J. Evolution 39, 783–791.
Gatesy, J., Milinkovitch, M.C., Waddell, V., Stanhope, M., 1999. Syst. Biol. 48, 6–20.
Hergé, 1960. Tintin in Tibet, English version. Casterman, Belgium.
Kishino, H., Hasegawa, M.J., 1989. Mol. Evol. 29, 170–179.
Kocher, T.D. et al., 1989. Proc. Natl. Acad. Sci. USA 86, 6196–6200.
Löytynoja, A., Milinkovitch, M.C., 2001. SOAP, a program for cleaning multiple alignments from unstable blocks. Bioinformatics 17, 573–574.
Matthiessen, P., 1979. The Snow Leopard. Chatto & Windus, UK.
Matthiessen, P., Laird, T., 1995. East of Lo Monthong: In the Land of the Mustang. Shambhala Publishers, Boston, MA.
Swofford, D.L., 1997. PAUP*: Phylogenetic Analysis Using Parsimony (and other methods), version 4.0b4a. Sinauer Associates, Sunderland, MA.

View publication stats